

Figure 2 - CI-2-like sequences

1. Seq. ID No. 35, *Hordeum vulgare* (gi:68800)
2. Seq. ID No. 36, *Hordeum vulgare* (Y08625)
3. Seq. ID No. 37, *Zea mays* (gi:475922)
4. Seq. ID No. 38, *Vicia faba* (A21463)
5. Seq. ID No. 39, *Cucurbita maxima* (S55591, S12897)
6. Seq. ID No. 40, *Canavalia lineata* (JC2380)
7. Seq. ID No. 41, *Vigna angularis* (JX0089)
8. Seq. ID No. 42, *Nicotiana tabacum* (gi:19913)
9. Seq. ID No. 43, *Nicotiana glauca* (A56555)
10. Seq. ID No. 44, *Sambucus nigra* (Z46949)
11. Seq. ID No. 45, *Momordica charantia* (JC2508)
12. Seq. ID No. 46, *Cucurbita maxima* (S12897)
13. Seq. ID No. 47, *Solanum tuberosum* (P01052, U30861)
14. Seq. ID No. 48, *Solanum tuberosum* (U30861)
15. Seq. ID No. 49, *Lycopersicon peruvianum* (A39547)
16. Seq. ID No. 50, *Lycopersicon esculentum* (A32067, A24048)
17. Seq. ID No. 51, *Lycopersicon esculentum* (A24048)
18. Seq. ID No. 52, *Amaranthus caudatus* (S40496)
19. Seq. ID No. 53, *Arabidopsis thaliana* (AC005770)

2. Please replace the paragraph spanning lines 21-22 on page 6 of the specification with the following:

Barley High Lysine 6 (BHL6) is coded for by the polypeptides of Seq. ID No. 18 which is encoded for by the nucleic acid of Seq. ID No. 17.

3. Please replace the paragraph spanning lines 16 to 31 on page 8 of the specification with the following:

A "CI-2 like" polypeptide refers to a polypeptide of at least 23 consecutive amino acids of Seq. ID No. 2 or 4; or a polypeptide of at least 30% amino acid sequence identity with corresponding region of Seq. ID Nos. 2 or 4 or 20; or a CI-2-like polypeptide with modifications identified in CI-2; or a protease inhibitor with an active site loop typically between 53 and 70; or a CI-2 homologue modified to enhance its nutritional value by altering the amino acid residues at positions corresponding to those defined herein. The following organisms may be modified according to the methods and figures in the specification *Hordeum vulgare* (Seq. ID No. 35), *Hordeum*

vulgare (Seq. ID No. 36), Zea mays (Seq. ID No. 37), Vicia faba (Seq. ID No. 38), Cucurbita maxima (Seq. ID No. 39), Canavalia lineata (Seq. ID No. 40), Vigna angularis (Seq. ID No. 41), Nicotiana tabacum (Seq. ID No. 42), Nicotiana glauca (Seq. ID No. 43), Sambucus nigra (Seq. ID No. 44), Momordica charantia (Seq. ID No. 45), Cucurbita maxima (Seq. ID No. 46), Solanum tuberosum (Seq. ID No. 47), Solanum tuberosum (Seq. ID No. 48), Lycopersicon peruvianum (Seq. ID No. 49), Lycopersicon esculentum (Seq. ID No. 50), Lycopersicon esculentum (Seq. ID No. 51), Amaranthus caudatus (Seq. ID No. 52), Arabidopsis thaliana (Seq. ID No. 53).

4. Please replace the paragraph spanning lines 12 to 17 on page 12 of the specification with the following:

"Methods of alignment of sequences for comparison are well-known in the art. For purposes of defining the present invention, the BLAST 2.0 suite of programs using default parameters is used. Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997). Software for performing BLAST analyses is publicly available, e.g., such software may be retrieved from the National Center for Biotechnology Information over the Internet <URL:http://www.ncbi.nlm.nih.gov>.

5. Please replace the Abstract of the Disclosure on p. 76 of the specification with the following:

The invention provides isolated nucleic acids and their encoded polypeptides that are involved in enhancing the essential amino acid content of a plant. The polypeptide may be derived from a protease inhibitor, and more specifically, a chymotrypsin inhibitor. Chymotrypsin inhibitors that may be modified for use in the invention are present in many plant species, including barley. Optionally there is also a decrease in protease inhibitory activity of the polypeptide. The invention further